

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/593,842

Source: IFWP

Date Processed by STIC: 10/3/06

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IFWP

RAW SEQUENCE LISTING

DATE: 10/03/2006

PATENT APPLICATION: US/10/593,842

TIME: 09:00:37

Input Set : A:\082368-000510US.txt

Output Set: N:\CRF4\10032006\J593842.raw

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3 <110> APPLICANT: Nakamura, Yusuke
4     Daigo, Yataro
5     Nakatsuru, Shuichi
7 <120> TITLE OF INVENTION: METHOD FOR DIAGNOSING NON-SMALL CELL
8     LUNG CANCER
10 <130> FILE REFERENCE: 082368-000510US
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/593,842
C--> 12 <141> CURRENT FILING DATE: 2006-09-22
12 <150> PRIOR APPLICATION NUMBER: PCT/JP2005/005613
13 <151> PRIOR FILING DATE: 2005-03-18
15 <150> PRIOR APPLICATION NUMBER: US 60/555,789
16 <151> PRIOR FILING DATE: 2004-03-23
18 <160> NUMBER OF SEQ ID NOS: 127
20 <170> SOFTWARE: PatentIn version 3.3
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 4908
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (141)..(3311)
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37 attttttggc ggggaccgtc atg gcg tcg cag cca aat tcg tct gcg aag aag      173
38             Met Ala Ser Gln Pro Asn Ser Ser Ala Lys Lys
39             1             5             10
41 aaa gag gag aag ggg aag aac atc cag gtg gtg gtg aga tgc aga cca      221
42 Lys Glu Glu Lys Gly Lys Asn Ile Gln Val Val Val Arg Cys Arg Pro
43             15             20             25
45 ttt aat ttg gca gag cgg aaa gct agc gcc cat tca ata gta gaa tgt      269
46 Phe Asn Leu Ala Glu Arg Lys Ala Ser Ala His Ser Ile Val Glu Cys
47             30             35             40
49 gat cct gta cga aaa gaa gtt agt gta cga act gga gga ttg gct gac      317
50 Asp Pro Val Arg Lys Glu Val Ser Val Arg Thr Gly Gly Leu Ala Asp
51             45             50             55
53 aag agc tca agg aaa aca tac act ttt gat atg gtg ttt gga gca tct      365
54 Lys Ser Ser Arg Lys Thr Tyr Thr Phe Asp Met Val Phe Gly Ala Ser
55 60             65             70             75
57 act aaa cag att gat gtt tac cga agt gtt gtt tgt cca att ctg gat      413
58 Thr Lys Gln Ile Asp Val Tyr Arg Ser Val Val Cys Pro Ile Leu Asp
59             80             85             90
61 gaa gtt att atg ggc tat aat tgc act atc ttt gcg tat ggc caa act      461

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62	Glu	Val	Ile	Met	Gly	Tyr	Asn	Cys	Thr	Ile	Phe	Ala	Tyr	Gly	Gln	Thr	
63				95					100					105			
65	ggc	act	gga	aaa	act	ttt	aca	atg	gaa	ggt	gaa	agg	tca	cct	aat	gaa	509
66	Gly	Thr	Gly	Lys	Thr	Phe	Thr	Met	Glu	Gly	Glu	Arg	Ser	Pro	Asn	Glu	
67			110					115					120				
69	gag	tat	acc	tgg	gaa	gag	gat	ccc	ttg	gct	ggt	ata	att	cca	cgt	acc	557
70	Glu	Tyr	Thr	Trp	Glu	Glu	Asp	Pro	Leu	Ala	Gly	Ile	Ile	Pro	Arg	Thr	
71		125					130					135					
73	ctt	cat	caa	att	ttt	gag	aaa	ctt	act	gat	aat	ggt	act	gaa	ttt	tca	605
74	Leu	His	Gln	Ile	Phe	Glu	Lys	Leu	Thr	Asp	Asn	Gly	Thr	Glu	Phe	Ser	
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77	gtc	aaa	gtg	tct	ctg	ttg	gag	atc	tat	aat	gaa	gag	ctt	ttt	gat	ctt	653
78	Val	Lys	Val	Ser	Leu	Leu	Glu	Ile	Tyr	Asn	Glu	Glu	Leu	Phe	Asp	Leu	
79				160						165				170			
81	ctt	aat	cca	tca	tct	gat	gtt	tct	gag	aga	cta	cag	atg	ttt	gat	gat	701
82	Leu	Asn	Pro	Ser	Ser	Asp	Val	Ser	Glu	Arg	Leu	Gln	Met	Phe	Asp	Asp	
83			175						180					185			
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86	Pro	Arg	Asn	Lys	Arg	Gly	Val	Ile	Lys	Gly	Leu	Glu	Glu	Ile	Thr		
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94	Lys	Arg	Thr	Thr	Ala	Ala	Thr	Leu	Met	Asn	Ala	Tyr	Ser	Ser	Arg	Ser	
95	220				225					230				235			
97	cac	tca	gtt	ttc	tct	gtt	aca	ata	cat	atg	aaa	gaa	act	acg	att	gat	893
98	His	Ser	Val	Phe	Ser	Val	Thr	Ile	His	Met	Lys	Glu	Thr	Thr	Ile	Asp	
99			240						245				250				
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102	Gly	Glu	Glu	Leu	Val	Lys	Ile	Gly	Lys	Leu	Asn	Leu	Val	Asp	Leu	Ala	
103			255					260					265				
105	gga	agt	gaa	aac	att	ggc	cgt	tct	gga	gct	gtt	gat	aag	aga	gct	cgg	989
106	Gly	Ser	Glu	Asn	Ile	Gly	Arg	Ser	Gly	Ala	Val	Asp	Lys	Arg	Ala	Arg	
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114	Thr	Ala	Leu	Val	Glu	Arg	Thr	Pro	His	Val	Pro	Tyr	Arg	Glu	Ser	Lys	
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118	Leu	Thr	Arg	Ile	Leu	Gln	Asp	Ser	Leu	Gly	Gly	Arg	Thr	Arg	Thr	Ser	
119			320					325					330				
121	ata	att	gca	aca	att	tct	cct	gca	tct	ctc	aat	ctt	gag	gaa	act	ctg	1181
122	Ile	Ile	Ala	Thr	Ile	Ser	Pro	Ala	Ser	Leu	Asn	Leu	Glu	Glu	Thr	Leu	
123			335					340					345				
125	agt	aca	ttg	gaa	tat	gct	cat	aga	gca	aag	aac	ata	ttg	aat	aag	cct	1229
126	Ser	Thr	Leu	Glu	Tyr	Ala	His	Arg	Ala	Lys	Asn	Ile	Leu	Asn	Lys	Pro	

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133	gag gag ata gaa cgt tta aaa cga gat ctt gct gca gcc cgt gag aaa	1325		
134	Glu Glu Ile Glu Arg Leu Lys Arg Asp Leu Ala Ala Arg Glu Lys			
135	380 385 390 395			
137	aat gga gtg tat att tct gaa gaa aat ttt aga gtc atg agt gga aaa	1373		
138	Asn Gly Val Tyr Ile Ser Glu Glu Asn Phe Arg Val Met Ser Gly Lys			
139	400 405 410			
141	tta act gtt caa gaa gag cag att gta gaa ttg att gaa aaa att ggt	1421		
142	Leu Thr Val Gln Glu Glu Gln Ile Val Glu Leu Ile Glu Lys Ile Gly			
143	415 420 425			
145	gct gtt gag gag gag ctg aat agg gtt aca gag ttg ttt atg gat aat	1469		
146	Ala Val Glu Glu Glu Leu Asn Arg Val Thr Glu Leu Phe Met Asp Asn			
147	430 435 440			
149	aaa aat gaa ctt gac cag tgt aaa tct gac ctg caa aat aaa aca caa	1517		
150	Lys Asn Glu Leu Asp Gln Cys Lys Ser Asp Leu Gln Asn Lys Thr Gln			
151	445 450 455			
153	gaa ctt gaa acc act caa aaa cat ttg caa gaa act aaa tta caa ctt	1565		
154	Glu Leu Glu Thr Thr Gln Lys His Leu Gln Glu Thr Lys Leu Gln Leu			
155	460 465 470 475			
157	gtt aaa gaa gaa tat atc aca tca gct ttg gaa agt act gag gag aaa	1613		
158	Val Lys Glu Glu Tyr Ile Thr Ser Ala Leu Glu Ser Thr Glu Glu Lys			
159	480 485 490			
161	ctt cat gat gct gcc agc aag ctg ctt aac aca gtt gaa gaa act aca	1661		
162	Leu His Asp Ala Ala Ser Lys Leu Leu Asn Thr Val Glu Glu Thr Thr			
163	495 500 505			
165	aaa gat gta tct ggt ctc cat tcc aaa ctg gat cgt aag aag gca gtt	1709		
166	Lys Asp Val Ser Gly Leu His Ser Lys Leu Asp Arg Lys Lys Ala Val			
167	510 515 520			
169	gac caa cac aat gca gaa gct cag gat att ttt ggc aaa aac ctg aat	1757		
170	Asp Gln His Asn Ala Glu Ala Gln Asp Ile Phe Gly Lys Asn Leu Asn			
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173	agt ctg ttt aat aat atg gaa gaa tta att aag gat ggc agc tca aag	1805		
174	Ser Leu Phe Asn Asn Met Glu Glu Leu Ile Lys Asp Gly Ser Ser Lys			
175	540 545 550 555			
177	caa aag gcc atg cta gaa gta cat aag acc tta ttt ggt aat ctg ctg	1853		
178	Gln Lys Ala Met Leu Glu Val His Lys Thr Leu Phe Gly Asn Leu Leu			
179	560 565 570			
181	tct tcc agt gtc tct gca tta gat acc att act aca gta gca ctt gga	1901		
182	Ser Ser Ser Val Ser Ala Leu Asp Thr Ile Thr Thr Val Ala Leu Gly			
183	575 580 585			
185	tct ctc aca tct att cca gaa aat gtg tct act cat gtt tct cag att	1949		
186	Ser Leu Thr Ser Ile Pro Glu Asn Val Ser Thr His Val Ser Gln Ile			
187	590 595 600			
189	ttt aat atg ata cta aaa gaa caa tca tta gca gca gaa agt aaa act	1997		
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193	gta cta cag gaa ttg att aat gta ctc aag act gat ctt cta agt tca	2045
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195	620 625 630 635	
197	ctg gaa atg att tta tcc cca act gtg gtg tct ata ctg aaa atc aat	2093
198	Leu Glu Met Ile Leu Ser Pro Thr Val Val Ser Ile Leu Lys Ile Asn	
199	640 645 650	
201	agt caa cta aag cat att ttc aag act tca ttg aca gtg gcc gat aag	2141
202	Ser Gln Leu Lys His Ile Phe Lys Thr Ser Leu Thr Val Ala Asp Lys	
203	655 660 665	
205	ata gaa gat caa aaa aag gaa cta gat ggc ttt ctc agt ata ctg tgt	2189
206	Ile Glu Asp Gln Lys Lys Glu Leu Asp Gly Phe Leu Ser Ile Leu Cys	
207	670 675 680	
209	aac aat cta cat gaa cta caa gaa aat acc att tgt tcc ttg gtt gag	2237
210	Asn Asn Leu His Glu Leu Gln Glu Asn Thr Ile Cys Ser Leu Val Glu	
211	685 690 695	
213	tca caa aag caa tgt gga aac cta act gaa gac ctg aag aca ata aag	2285
214	Ser Gln Lys Gln Cys Gly Asn Leu Thr Glu Asp Leu Lys Thr Ile Lys	
215	700 705 710 715	
217	cag acc cat tcc cag gaa ctt tgc aag tta atg aat ctt tgg aca gag	2333
218	Gln Thr His Ser Gln Glu Leu Cys Lys Leu Met Asn Leu Trp Thr Glu	
219	720 725 730	
221	aga ttc tgt gct ttg gag gaa aag tgt gaa aat ata cag aaa cca ctt	2381
222	Arg Phe Cys Ala Leu Glu Glu Lys Cys Glu Asn Ile Gln Lys Pro Leu	
223	735 740 745	
225	agt agt gtc cag gaa aat ata cag cag aaa tct aag gat ata gtc aac	2429
226	Ser Ser Val Gln Glu Asn Ile Gln Gln Lys Ser Lys Asp Ile Val Asn	
227	750 755 760	
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231	765 770 775	
233	tca cag gaa ctc aga aat ttt aac caa gaa ggt aca aaa ttg gtt gaa	2525
234	Ser Gln Glu Leu Arg Asn Phe Asn Gln Glu Gly Thr Lys Leu Val Glu	
235	780 785 790 795	
237	gaa tct gtg aaa cac tct gat aaa ctc aat ggc aac ctg gaa aaa ata	2573
238	Glu Ser Val Lys His Ser Asp Lys Leu Asn Gly Asn Leu Glu Lys Ile	
239	800 805 810	
241	tct caa gag act gaa cag aga tgt gaa tct ctg aac aca aga aca gtt	2621
242	Ser Gln Glu Thr Glu Gln Arg Cys Glu Ser Leu Asn Thr Arg Thr Val	
243	815 820 825	
245	tat ttt tct gaa cag tgg gta tct tcc tta aat gaa agg gaa cag gaa	2669
246	Tyr Phe Ser Glu Gln Trp Val Ser Ser Leu Asn Glu Arg Glu Gln Glu	
247	830 835 840	
249	ctt cac aac tta ttg gag gtt gta agc caa tgt tgt gag gct tca agt	2717
250	Leu His Asn Leu Leu Glu Val Val Ser Gln Cys Cys Glu Ala Ser Ser	
251	845 850 855	
253	tca gac atc act gag aaa tca gat gga cgt aag gca gct cat gag aaa	2765
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255	860 865 870 875	
257	cag cat aac att ttt ctt gat cag atg act att gat gaa gat aaa ttg	2813

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261 ata gca caa aat cta gaa ctt aat gaa acc ata aaa att ggt ttg act      2861
262 Ile Ala Gln Asn Leu Glu Leu Asn Glu Thr Ile Lys Ile Gly Leu Thr
263      895      900      905
265 aag ctt aat tgc ttt ctg gaa cag gat ctg aaa ctg gat atc cca aca      2909
266 Lys Leu Asn Cys Phe Leu Glu Gln Asp Leu Lys Leu Asp Ile Pro Thr
267      910      915      920
269 ggt acg aca cca cag agg aaa agt tat tta tac cca tca aca ctg gta      2957
270 Gly Thr Thr Pro Gln Arg Lys Ser Tyr Leu Tyr Pro Ser Thr Leu Val
271      925      930      935
273 aga act gaa cca cgt gaa cat ctc ctt gat cag ctg aaa agg aaa cag      3005
274 Arg Thr Glu Pro Arg Glu His Leu Leu Asp Gln Leu Lys Arg Lys Gln
275 940      945      950      955
277 cct gag ctg tta atg atg cta aac tgt tca gaa aac aac aaa gaa gag      3053
278 Pro Glu Leu Leu Met Met Leu Asn Cys Ser Glu Asn Asn Lys Glu Glu
279      960      965      970
281 aca att ccg gat gtg gat gta gaa gag gca gtt ctg ggg cag tat act      3101
282 Thr Ile Pro Asp Val Asp Val Glu Glu Ala Val Leu Gly Gln Tyr Thr
283      975      980      985
285 gaa gaa cct cta agt caa gag cca tct gta gat gct ggt gtg gat tgt      3149
286 Glu Glu Pro Leu Ser Gln Glu Pro Ser Val Asp Ala Gly Val Asp Cys
287      990      995      1000
289 tca tca att ggc ggg gtt cca ttt ttc cag cat aaa aaa tca cat      3194
290 Ser Ser Ile Gly Gly Val Pro Phe Phe Gln His Lys Lys Ser His
291      1005      1010      1015
293 gga aaa gac aaa gaa aac aga ggc att aac aca ctg gag agg tct      3239
294 Gly Lys Asp Lys Glu Asn Arg Gly Ile Asn Thr Leu Glu Arg Ser
295      1020      1025      1030
297 aaa gtg gaa gaa act aca gag cac ttg gtt aca aag agc aga tta      3284
298 Lys Val Glu Glu Thr Thr Glu His Leu Val Thr Lys Ser Arg Leu
299      1035      1040      1045
301 cct ctg cga gcc cag atc aac ctt taa ttcacttggg ggttggcaat      3331
302 Pro Leu Arg Ala Gln Ile Asn Leu
303      1050      1055
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325 agcttaacat aggtaaatat caccaacatc tgctccttaga aaggaccatc tcatgttttt      3991
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329 tcctcggtc actttctccc tttttatttt tcaccaaacc atttgtagag ctacaaaacc      4111
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31
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VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date